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Subsequently, an End Rescue Site was ligated into the EcoRI site. Hereto, two oligonucleotides (strand 1: 5'-TTCGGATCCGGTACCATCGAT-3' (SEQ ID NO:161) AND STRAND 2: 3'GCCTAGGCCATGGTAGCTATT-5' (SEQ ID NO:162) were ligated into a partial (dATP) filled ECORI site, generating the vector pDF1. Triplet repeat containing fragmentation vectors were constructed by cloning of a 21bp and a 30bp CAG/CTG adapter into the Klenow-filled PstI site of pDF1. Transformation and selection resulted in a (CAG)₇ and a (CTG)₁₀ fractionation vector with the orientation of the repeat sequence 5' to 3' relative to the telomere.

Remarks

Applicants file a substitute Sequence Listing herewith to correct the inadvertent omission of sequences from the previously filed Sequence listing. Applicants have also amended the specification to include sequence identification numbers that were inadvertently omitted from the application as originally filed. No new matter has been added.

Applicants respectfully request reconsideration of the specification in view of the amendments made above. If the Examiner wishes to advance the prosecution, or if the amendment is defective or unclear in some way, then the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

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Attorney Docket No. B00192/70019 (JRV/MXA)

Date: August 1, 2002

X08/01/02

Marked-up Specification

Page 22, line 23 through Page 23 line 20:

FIGURE 1 shows a sequence of nucleotides which is the left arm end-sequence of YAC 766_f_12; {(SEQ ID NO: 1).}

FIGURE 2 shows a sequence of nucleotides which is a right arm end-sequence of YAC 766_f_12; {(SEQ ID NO: 2).}

FIGURE 3 shows a sequence of nucleotides which is the left arm end-sequence of YAC 717_d_3; {(SEQ ID NO:3).}

FIGURE 4 shows a sequence of nucleotides which is the right arm end-sequence of YAC 717_d_3; {(SEQ ID NO:4).}

FIGURE 5 shows a sequence of nucleotides which is the right arm end-sequence of YAC 731_c_7; {(SEQ ID NO:5).}

FIGURE 6 shows a sequence of nucleotides which is the left arm end-sequence of YAC 752_g_8; {(SEQ ID NO:6).}

FIGURE 7 shows a sequence of nucleotides which is the left arm end-sequence of YAC 942_c_3; {(SEQ ID NO:7).}

FIGURE 8 shows a sequence of nucleotides which is the right arm end-sequence of YAC 942_c_3; {(SEQ ID NO:8).}

FIGURE 9 shows a sequence of nucleotides which is the left arm end-sequence of YAC 961_h_9; {(SEQ ID NO:9).}

FIGURE 10 shows a sequence of nucleotides which is the right arm end-sequence of YAC 961_h_9; {(SEQ ID NO:10).}

FIGURE 11 shows a sequence of nucleotides which is the left arm end-sequence of YAC 907_e_1; {(SEQ ID NO:11).}

Page 23, line 35 through page 24, line 26:

FIGURE 15 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 961_h_9 {(SEQ ID NO:12)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs:13 and 14)}.

FIGURE 16 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 766_f_12 {(SEQ ID NO: 15)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs:16 and 17)}.

FIGURE 17 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 766_f_12 {(SEQ ID NO: 18)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs: 19 and 20)}.

FIGURE 18 shows (a) a CTG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 907_e_1 {(SEQ ID NO: 21)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs:22 and 23)}.

Page 36 line 1 through Page 61 line 22:

D18S60:

Database ID: AFM178XE3 (Also known as 178xe3, Z16781, D18S60)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:

Left = CCTGGCTCACCTGGCA {(SEQ ID NO:24)}
Right = TTGTAGCATCGTTGTAATGTTCC {(SEQ ID NO:25)}
Product Length = 157

Review complete sequence:

AGCTATCCTGGCTCACCTGGCAAAAATACAGTGTATACACACACACACACACAC
ACACACACACACAGAGTGTNTTANTNATTCCAGCAAATAATATTACATATAAAAGA
TCTAATTGGTTCATCATGTAAATTTAGTAGGAACATTACAACGATGCTACAAGANTT
TATCCAAACTGAGATTTCTTAGAATATCTGTTAAAAGTAATTTTATTCAGTTAATA
GAAATTCTATTGAAAACATCAAACCTATAAAGCT {(SEQ ID NO:26)}

Genbank ID: Z16781

Description: H. sapiens (D18S60) DNA segment containing (CA) repeat; clone
Search for GDB entry

WI-9222:

Database ID: UTR-03540 (Also known as G06101, D18S1033, 9222, X63657)
Source: WICGR: Primers derived from Genbank sequences
Chromosome: Chr18

Primers:

Left = GATCCCATAAAGCTACGAGGG {(SEQ ID NO:27)}
Right = GAGTCTAAAGACAAGAAAGCATTGC {(SEQ ID NO:28)}
Product Length = 99

Review complete sequence:

TCTTCTTACCCCTTGGAAGAAGACTGTTTCCAAATAATTTGAACAGCTTGCTGCTAA
ATGGGACCCAATTTTTGGCCTATAGACACTTATGTATTGTTTTCGAATACGTCAGATT
GGACCAGTGCTCTTCAGGAATGTGGCTGCAAGCAAGGGGCTAGAAGTTCACCTCCT
GACAGTATTATTAATACTATGCAAATATGGAATAGGAGACCATTGATTTTCTAGGC
TTTGTGGTAGAGAGGTGAAGGTATGAGAATTAATAGCGTGTGAACAAAGTAAAGAA
CAGGATTCCAGAATGATCATTAAATTTGTTTCTATTTATTCTTTTTTGCCCCCTAGA
GATTAAGTCCAGAAATGTACTTTCTGGCACATAAAGAAATCTTGAGGACTTTGTTTA
AACCTTCCATAAAAAACAATTTTCGGTTTCTCGGGTNNNNNNNNNNNNNNNNNNNN
NNNTTCTTTCTTTG
TGTATTTTATTCAAGATGAGTTGGACCCATTGCCAGTGAGTCTGAATGTCACTGACA
GCCCTGTGTTGTGCTCAGGACTCACTCTGCTGCTGGTGGAACTCATGGCTTCTCTCT
CTCTTTGATCCCATAAAGCTACGAGGGGGACGGGAGAGGGCAGTGCAATGGGAAGT
AAAGAGATATTTCCAGTAGGAAAAGCAATGCTTTCTTGTCTTTAGACTCAAATGCT
TAGGGAACGTTTCATTTCTCATTTCATGGGGAAAGGCAGCCTCCTTAAATGTTTTCTG
AAGAGCGGTAAATCTAGAAGCTTAAGAATTTACAGTTCCTTCAATAACCATGATGA
CCTGAAGTTCACCTATCCCATTTTAGCATCTACTTGTTTTTCCCATCTCTTCCTTTCCA

ATTTTGCTTATACTGCTGTAATATTTTGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNG
ACCAGCTAAAATTTTCGACTTGACTTTTTAACTTAACTCATGAATTAATTAAAGCAA
ATGAAAAAATTAAAAAGTGTGACTTTTTCTCGGAGCATATATGTAGCTTTTAGGAAA
GGCTGATGATGGTATAAAGTTTGCTCATTAAGAAAAAAGACAAGGCTGATTTTGA
AGAGAGTTGCTTTTGAAATAAAATGATCA {(SEQ ID NO:29)}

Genbank ID: X63657

Description: H.sapiens fvt1 mRNA

Search for GDB entry

WI-7336:

Database ID: UTR-04664 (Also known as PI5, G00-679-135, G06527, 7336, U04313)

Source: WICGR: Primers derived from Genbank sequences

Chromosome: Chr18

Primers:

Left = AGACATTCTCGCTTCCCTGA {(SEQ ID NO:30)}

Right = AATTTTGACCCCTTATGGGC {(SEQ ID NO:31)}

Product Length = 332

Review complete sequence:

TAAGTGGCATAGCCCATGTAAAGTCCTCCCTGACTTTTCTGTGGATGCCGATTTCTGT
AAACTCTGCATCCAGAGATTCATTTTCTAGATACAATAAATTGCTAATGTTGCTGGA
TCAGGAAGCCGCCAGTACTTGTTCATATGTAGCCTTCACACAGATAGACNNNNNNN
NNNNCCAATTCTATCTTTTGTTCCTTTTTTCCCATAAGACAATGACATACGCTTTTA
ATGAAAAGGAATCACGTTAGAGGAAAAATATTTATTCATTATTTGTCAAATTGTCCG
GGGTAGTTGGCAGAAATACAGTCTTCCACAAAGAAAATTCCTATAAGGAAGATTTG
GAAGCTCTTCTTCCCAGCACTATGCTTTCCTTCTTTGGGATAGAGAATGTTCCAGACA
TTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCC
CTGGCTCCAGTGAAACTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAGTCCTTA
TGTTAAGCCCTGGCAGGCAGGTGTTTATTAATAAATTCTGAATTTTGGGGATTTTCAA
AGATAATATTTTACATACACTGTATGTTATAGAAGTTCATGGATCAGATCTGGGGCA
GCAACCTATAAATCAACACCTTAATATGCTGCAACAAAATGTAGAATATTCAGACA
AAATGGATACATAAAGACTAAGTAGCCCATAGGGGTCAAAATTTGCTGCCAAATG
CGTATGCCACCAACTTACAAAAACACTTCGTTCCGACAGAGCTTTTCAGATTGTGGAAT
GTTGGATAAGGAATTATAGACCTCTAGTAGCTGAAATGCAAGACCCCAAGAGGAAG
TTCAGATCTTAATATAAATTCATTTTCTATGATAGCTGTCCCATCTGGTCATGTG
GTTGGCACTAGACTGGTGGCAGGGGCTTCTAGCTGACTCGCACAGGGATTCTCACAA
TAGCCGATATCAGAATTTGTGTTGAAGGAAGTGTCTCTTCATCTAATATGATAGCG
GGAAAAGGAGAGGAACTACTGCCTTTAGAAAATATAAGTAAAGTGATTAAAGTGC
TCACGTTACCTTGACACATAGTTTTTTCAGTCTATGGGTTTAGTTACTTTAGATGGCAA
GCATGTAAGTTATATTAATAGTAATTTGTAAAGTTGGGTGGATAAGCTATCCCTGTT
GCCGGTTCATGGATTACTTCTCTATAAAAAATATATATTTACCAAAAAATTTTGTGA
CATTCCTTCTCCCATCTCTTCTTCTGACATGCATTGTAAATAGGTTCTTCTTGTCTGAG

ATTCAATATTGAATTTCTCCTATGCTATTGACAATAAAATATTATTGAACTACC
{(SEQ ID NO:32)}

Genbank ID: G06527

Description: WICGR: Random genome wide STSs

X

WI-8145:

Database ID: EST102441 (Also known as D18S1234, G00-677-827, G06845, 8145, T49159)

Source: WICGR: STSs derived from dbEST sequences

Chromosome: Chr18

Primers:

Left = GAAATGCACATAACATATATTTGCC {(SEQ ID NO:33)}

Right = TGCTCACTGCCTATTTAATGTAGC {(SEQ ID NO:34)}

Product Length = 184

Review complete sequence:

GTTGTTTGGANGCAGGTTTATTTATTATATACTTGCAATTGAATATAAGATACAGAC
ATATATATGTGTTATGTATTTCTAGAAATGCACATAACATATATTTGCCTATTGTTTA
ATGTTTTTTCCAGANATTTATTACAGAAGGGCATGGAGGGATACCTACTTATTCTTC
ATTATGAGAACAATTAAAGGCATTTATTAGATAGGAAATTAACAGANCATCTGCTTC
TATAACTTTATTAGCTACATTAAATAGGCAGTGAGCANTAATTTAAANCTCACCAT
TATATAAANTANTAAATACCAAAGTAAAAG {(SEQ ID NO:35)}

_____ : left and right primer

PCR Conditions

Genbank ID: T49159

Description: yb09e07.s1 Homo sapiens cDNA clone 70692 3' similar to gb:J02685

UniGene Cluster Description: Human mRNA for Arg-Serpin (plasminogen activator-inhibitor 2, PAI-2) Search for GDB entry

WI-7061:

Database ID: UTR-02902 (Also known as PAI2, G00-678-979, G06377, 7061, M18082)

Source: WICGR: Primers derived from Genbank sequences

Chromosome: Chr18

Primers:

Left = TGCTCTTCTGAACAACTTCTGC {(SEQ ID NO:36)}

Right = ATAGAAGGGCATGGAGGGAT {(SEQ ID NO:37)}

Product Length = 338

Review complete sequence:

AACTAAGCGTGCTGCTTCTGCAAAAGATTTTTGTAGATGAGCTGTGTGCCTCAGAAT
TGCTATTTCAAATTGCCAAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGA
ACAACTTCTGCTACCCACTAAATAAAAAACACAGAAATAATTAGACAATTGTCTATTA
TAACATGACAACCCTATTAATCATTGGTCTTCTAAAATGGGATCATGCCCATTTAG
ATTTTCCTTACTATCAGTTTATTTTTATAACATTAACCTTTTACTTTGTTATTTATTATT
TATATAATGGTGAGTTTTAAATTATTGCTCACTGCCTATTTAATGTAGCTAATAAAGT
TATAGAAGCAGATGATCTGTTAATTTCTATCTAATAAATGCCTTTAATTGTTCTCAT
AATGAAGAATAAGTAGGTATCCCTCCATGCCCTTCTATAATAAATATCTGGAAAAAA
CATTAAACAATAGGCAAATATATGTTATGTGCATTTCTAGAAATACATAACACATAT
ATATGTCTGTATCTTATATTCAATTGCAAGTATATAATAAATAAACCTGCTTCCAAAC
AACNNNNNNNNNNNNNNNGGAATTC {(SEQ ID NO:38)}

PCR Conditions

Genbank ID: G06377

Description: WICGR: Random genome wide STSs

D18S68:

Database ID: AFM248YB9 (Also known as 248yb9, Z17122, D18S68)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = ATGGGAGACGTAATACACCC {(SEQ ID NO:39)}

Right = ATGCTGCTGGTCTGAGG {(SEQ ID NO:40)}

Product Length = 285

Review complete sequence:

AAAGAGTTGGGGTTGTGAATTCCACACACAGTCAACTATTGGCTATGGGCTTACCAT
GGGAGACGTAATACACCCGGNACTTCCAACTCACATACCAGAGACATGGCTCTAGC
ACCCAATGGAAATATGCTGAATGTTGCAGGTGCAAGACAGCAACAAAGCAGACAGA
GGCACATAGACAAGGCACCAACAGTGTCCACTATACCCTGACAGTGTGGAAAGTTG
TAGATAGGATGAAGAGAAAGAATACACACACACACACACACACACACACACAC
ACACACACACACACCGGTAGANACTTACTACNCAAAGTGTGANCCTCAGACCAGC
AGCATCTGGCNAAATGGTGATCTATCACCTTCCAG {(SEQ ID NO:41)}

Genbank ID: Z17122

Description: H. sapiens (D18S68) DNA segment containing (CA) repeat; clone

WI-3170:

Database ID: MR3726 (Also known as D18S1037, G04207, HALd22f2, 3170)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = TGTGCTACTGATTAAGGTAAAGGC {(SEQ ID NO:42)}

Right = TGCTTCTTCAATTTGTAGAGTTGG {(SEQ ID NO:43)}

Product Length = 156

Review complete sequence

CTGAGACAAGGCAGGCAAACAACCTCTAAAAATCTACAATTGGTGATTGGTGTGCT
ACTGATTAAGGTAAAGGCACAGAATTATACATCCAGGTTNCTATTACTTATGGCAGA
CTCAGGACCCAGGTTNAGAGACCACTGGCCTTAAGAAAAAAAAAATGGGGTTCCTGAT
TTCTGGATAATAATCCAACCTCTACAAATTGAAGAAGCAACATACCCTCTTTGTTA
{(SEQ ID NO:44)}

Genbank ID: G04207

Description: WICGR: Random genome wide STSs

WI-5654:

Database ID: MR10908 (Also known as D18S1259, G00-678-695, G05278, 5654)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = CTTAATGAAAACAATGCCAGAGC {(SEQ ID NO:45)}

Right = TGCAAAATGTGGAATAATCTGG {(SEQ ID NO:46)}

Product Length = 149

Review complete sequence:

CTACAAAATGCATGTGGCTTTGGCTTTGAAATAGTACACCCTATCAAAGACTAAATT
TTCTTAATGAAAACAATGCCAGAGCTTTTTTCATGATATTTTGTTTTATAGAGATGGGG
AACAATCTGGACGTTGTTTCCTTATCTGGGTGGTAATCGAGGCTTAGCAATTTCCCA
CAGCGTTACACAAATCCAGATTATTCCACATTTTGCAAATA {(SEQ ID NO:47)}

Genbank ID: G05278

Description: WICGR: Random genome wide STSs

D18S55:

Database ID: AFM122XC1 (Also known as 122xc1, Z16621, D18S55, GC378-D18S55)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = GGGAAGTCAAATGCAAAATC {(SEQ ID NO:48)}

Right = AGCTTCTGAGTAATCTTATGCTGTG {(SEQ ID NO:49)}

Product Length = 143

Review complete sequence:

AGCTGAACATGCCTTTTCATGGAGCAGTTTCNAAATACACTTTTGGTACAATCTGCA
GGTGGATATTTGGAGCTCAGGAGTTTGAGACCAGCCTGGGCAACATGGTGAAATCC
CGTCTCTACTAAAATACAAAAAATTAGCCAGGTGTGGCGGCATGTGCCTGTAGNCCC
AGGATGGATTGAGTGGGTGAGATATGGAATAAGTGGTGGGAAGTCAAATGCAAAAT
CAATTCAGTTTGTCAATATTGATTCTCTATTCTAGCCTGGCGTGGTTTTTCCTCGTCA
CAGCATAAGATT
ACTCAGAAGCT {(SEQ ID NO:50)}

Genbank ID: Z16621

Description: H. sapiens (D18S55) DNA segment containing (CA) repeat; clone

D18S969:

Database ID: GATA-P18099 (Also known as G08003, CHLC.GATA69F01,
CHLC.GATA69F01.P18099)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:

Left = AACAAGTGTGTATGGGGGTG {(SEQ ID NO:51)}

Right = CATATTCACCCAGTTTGTTC {(SEQ ID NO:52)}

Product Length = 365

Review complete sequence:

CAGGGAAATGCAAATCAAAACCACAATGAGTTATCTCCTCATACCTTTAATGATGGC
TAATATTAAACAAGAGATAACAAGTGTGTATGGGGGTGTGGAGAAAAGAGAATGTN
CGAACACTCTTGGTTGAAATATAAGTTGGTAGANCCATTATGCAAAACAGTATGAAT
CTTTATCAGTATAANATTAGGACCTNGCATATGATCNCAGCAATCNCCACNTCTGNG
NGATCNCACNCNCTATCTCTCTATATCTATCTATCTATCTATCTATCTATCTATCTATC
TATCTATCTATCTATCTATCTGTCTGTCTATCATCTATCTATCTTCTATCTATCTATCT
ATCTTTCTATCTATCTATCTGTCTATCTATNCCGGAATATTTTTCAGCCATNNAATA
AGGAAGTCCTGCTATTTGCAACAACTGGGTGAATATGGAGAACGTTATGCTAAAT
GCAATATGCTAAAGACAGACACAGAAAGACAAGTATGACCTCACTTATATGTGGAA
ACTGAAAAGCCATACTCATTACAGCAAAGAGTAGAATGTTGGTTACCAGGGGCAA
AGAGGGTAGAAATGAGGGGAGTGAGAAAATGTCAATCAAAGTGTAAGAATGTTATA
ACATAAATAAATTCATAGAG {(SEQ ID NO:53)}

Genbank ID: G08003

Description: human STS CHLC.GATA69F01.P18099 clone GATA69F01.

D18S1113:

Database ID: AFM200VG9 (Also known as D18S1113, 200vg9, w2403)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = GTTGACTCAAGTCCAAACCTG {(SEQ ID NO:54)}

Right = CAAAGACATTGTAGACGTTCTCTG {(SEQ ID NO:55)}

Product Length = 207

Review complete sequence:

AGCTGCATATAAACTATTCCATTTTACATTTTTGAAGACATTTGTAGCCATGATACT
TTGCTGTTGTCTGTGGGCCACCTCTTTTTGAAGTGTGTAGTTAACTGTGCTCCTGTAA
TCTGTTGTCTGTTGACTCAAGTCCAAACCTGTTCTGCGTGGCATGTTTCTNCAACTTG
ATGTGATGCTATTTATCACTTTCTTTGAAGTTAAGTCTCTATGTCTTTGTATTCTTTCT
GTGTACCCAGGGATATGTTTGTGCATGCACACGCATAAACACACACACACACACAC
ACACACACAGAGACAGAGACAGAGAACGTCTACAATGTCTTTGTGAG {(SEQ ID
NO:56)}

D18S868:

Database ID: GATA-D18S868 (Also known as G09150, CHLC.GATA3E12,
CHLC.GATA3E12.496, CHLC.496, D18S868)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:

Left = AGCCAATACCTTGTAGTAAATATCC {(SEQ ID NO:57)}

Right = GATTCTCCAGACAAATAATCCC {(SEQ ID NO:58)}

Product Length = 189

Review complete sequence:

GAGTGAGCCAATACCTTGTAGTAAATATCCATCTATCTTTGATGTATCTATGTATCTA
TCTTTGTATCTATATGTCTATGTATCTATGTATGTATGTATCTATCTATCATCTATCTA
TCTATCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCCNNTTTGGG
ATTATTTGTCTGGAGAATCCTGATTAACATAGTCTGCTAACTTTTATCTGTATCTCCT
ATGTGTATGCTTCTCCTTCTTCCTGTCTCTCTCTCTTCTTTGTCCTCATTTAANCTCCTT
TCCTGGGNATATTGGNAATTTTGATTGGANTCTGGACANTGTAGGAGTAAAAATTT
{(SEQ ID NO:59)}

Genbank ID: G09150

Description: human STS CHLC.GATA3E12.P6553 clone GATA3E12.

WI-9959:

Database ID: MR12816 (Also known as D18S1251, G00-678-524, G05488, 9959)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = TGCCAACAGCAGTCAAGC {(SEQ ID NO:60)}

Right = AGCACCTGCAGCAGTAATAGC {(SEQ ID NO:61)}

Product Length = 110

Review complete sequence:

CtgtttttattgaaaaaaaaaatctgtctccaagaagaaagttcattctACCTGTTGCCAACAGCAGTCAAGCGGA
CATGTTTAAAAATTTTTTAAAAAAGTATTTTTTTTCCAACTGGNGTTTAATAGCCTCA
TTTTGGCTTTTGCTATTACTGCTGCAGGTGCTTTNATTTTTTTCCTCTGCATTATAATT
AC {(SEQ ID NO:62)}

Genbank ID: G05488

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S537:

Database ID: CHLC.GATA2E06.13 (Also known as CHLC.13, GATA2E06, D18S537, GATA-D18S537)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:

Left = TCCATCTATCTTTGATGTATCTATG {(SEQ ID NO:63)}

Right = AGTTAGCAGACTATGTTAATCAGGA {(SEQ ID NO:64)}

Product Length = 191

Review complete sequence:

AAAGCTGAGTGAGCCAATACCTTGTAAGTAAATATCCATCTATCTTTGATGTATCTAT
GTATCTATCTTTGTATCTATATGTCTATGTATCTATGTATGTATCTATCTATCAT
CTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCC
NTTNGGTATTATTNGTCTGGNGAATCCTGATTAAACATAGTCTGCTAACTTNTATCTGT
ATCTNCTATGTGTATGCTTCTNCTTCTTCTGCTCTCTCTCTGCTTTGTCTCAATTN
AAATCTCC {(SEQ ID NO:65)}

Genbank ID: G07990

Description: human STS CHLC.GATA2E06.P6006 clone GATA2E06.

Search for GDB entry

D18S483:

Database ID: AFM324WC9 (Also known as 324wc9, Z24399, D18S483)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = TTCTGCACAATTTC AATAGATTC {(SEQ ID NO:66)}

Right = GAACTGAGCAAACGAGTATGA {(SEQ ID NO:67)}

Product Length = 214

Review complete sequence:

AGCTCTGCTGGAAGAGCAGGGCTGTTTTCTGCACAATTTCAATAGATTCCCCTACCC
TGGGTTTTTCAGTAGATAGATAGATAGATGATAGATAGGTAGATAGATAGATAGAT
AGATAGATAGATAGATAGATAGATGATAGATAGATTTTATATATAGTATATAAAATC
TACACACACACACACACACACACACACATATTTGCCTTTCCTTGACTATCATACT
CGTTTGCTCAGTTCTTTTTTTTTTTAAATTTTGTGTGTAATCCAAAATGCTT {(SEQ
ID NO:68)}

Genbank ID: Z24399

Description: H. sapiens (D18S483) DNA segment containing (CA) repeat; clone

Search for GDB entry

D18S465:

Database ID: AFM260YH1 (Also known as 260yh1, Z23850, D18S465)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = ATATTCCCCTATGGAAGTACAG {(SEQ ID NO:69)}

Right = AAAGTTAATTTTCAGGCACTCT {(SEQ ID NO:70)}

Product Length = 232

Review complete sequence:

AGCTCTGTCCCTCTAGAGAACGCTGACTAATATATTCCCCTATGGAAGTACAGATGG
TTTTNTAAAATAAATTTATCTGATTGTGATGAGATAATCATCATTTTTATGTTTCAGT
GTTTTCTAAATTTTTTATTGTTATTGTTTTTATACTCTAAATGGTTTTTAAATATGCA
CATATGTGCATATTTTACACACACACACACACACACACTCTCTTTATTTAGAA
GCATTATAGATAGAGTGCCTGAAAATTAACCTTTTAACCNAAGAAAAGACAATAAGG
AACAATAGGGAAGTTATCCTTTGCTAAGGGTATGGAAAATATTCACATATTATTTAT
AACANGTTAAACCAAGTCATGCTTGANTATAATAGCT {(SEQ ID NO:71)}

Genbank ID: Z23850

Description: H. sapiens (D18S465) DNA segment containing (CA) repeat; clone

Search for GDB entry

D18S968:

Database ID: GATA-P34272 (Also known as G10262, CHLC.GATA117C05,
CHLC.GATA117C05.P34272)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:

Primers:

Left = TCCTCTCATCTCGGATATGG {(SEQ ID NO:78)}

Right = AAGGCTTTCAGACTTACACTGG {(SEQ ID NO:79)}

Product Length = 394

Review complete sequence:

TTATTTATTCACTCATTCAATAAATATTTATGAATTCCTTTAATGGCNANGAAAGTA
TGTTTGGTACTGAATATGGTGAGCAAGATTTTCCTCTCATCTCGGATATGGAAAGAT
CTTGAAATCATTATACNTCATACTTACAATANGAAAGAAGCTGAGCAATTTGAAA
ATCAACAATTTCTTTTGTACNTGTCAGAAAAGTGAAGATATATTAATCAGGGTTCTT
CAGAGAAACATAACCAATAGGNCACAGNTCTATATGNCCNCNTTTATCTATCTATCT
ATCTATCTATCNCTATCTATCNANACCCNGGNGAANTNATNTTTGNGAGATTNATGC
AAGNCTGAGAAANACCNAAGAANCTGCTCCCTGTNAACTNGAGATNCAAGAANCT
GAANAGTATAGNTCCAGTCCNAAGTCTANAGACCTTAGAATTAGGAAAAGTATAC
TATAAATACCAGTGTAAGTCTGAAAGCCTTAAANACCANATAGTGCCATTGAAAGG
GCAGAAGACTGATGTCCAGTTCAAGCAGGCAAAGTTAGAGAAGCCTTATTTTCTGC
AACATTGTTCTATTCAGACCCTTNANANGATTGACNATGTCCACCCA {(SEQ ID
NO:80)}

Genbank ID: G08001

Description: human STS CHLC.GATA52H04.P16177 clone GATA52H04.

Search for GDB entry

WI-2620:

Database ID: MR1436 (Also known as G03602, D18S890, HHAa12h3, 2620)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = TCTCCAAGCTATTGATTGGATAA {(SEQ ID NO:81)}

Right = TTAAGAGCCAATTTATATAAAAGCAGC {(SEQ ID NO:82)}

Product Length = 177

Review complete sequence:

CCCCTTTTGCCAACGCCATGCTTCACGTAGGGAGCCTGACATGCAGAAAAGTCTCCA
AGCTATTGATTGGATAAAGAGCCAGAGCTGACTGAATTCCATTCTTCTTGAGCCTCT
CATTCTGTGTTTCTCGAATTTTACCAAAGCATCTTGACACACAAATATCTGACTCAA
GGAAAAGGAAAAACAACTGCTTTTCTCCAGCTGCTTTTATATAAATTGGCTCTTAA
ACTTTCTAAGTTTATTATGGATA {(SEQ ID NO:83)}

Genbank ID: G03602

Description: WICGR: Random genome wide STSs

Search for GDB entry

WI-4211:

Database ID: MR6638 (Also known as G03617, D18S980, 4211)
Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:

Left = ATGCTTCAGGATGACGTAATACA {(SEQ ID NO:84)}

Right = AAATTCTCGCTGATTGGAGG {(SEQ ID NO:85)}

Product Length = 113

Review complete sequence:

CTAGTACCATAATCCCTTTTGGGAATAAACCATCCCACCTTTAGTCAGANCAGATGCT
TCAGGATGACGTAATACATAATAAGCCTACTCAGTTCTACTCTGGCTTTGTATGTCTT
CAAAGTGATATTTTTTAAGTATTACTTGTCCCTCCAATCAGCGAGAATTT {(SEQ ID NO:86)}

Genbank ID: G03617

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S876:

Database ID: GATA-D18S876 (Also known as G09963, CHLC.GATA61E10, D18S876)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:

Left = TCAAACCTTATAACTGCAGAGAACG {(SEQ ID NO:87)}

Right = ATGGTAAACCCTCCCCATTA {(SEQ ID NO:88)}

Product Length = 171

Review complete sequence:

AAGACTGCAATTACATTTGCATCAAACCTTATAACTGCAGAGAACGTTGCCCACTATT
TTATACCACACAACAGTATTCTTAGCCAGATTACATCTATCTATCTATCTATCT
ATCTATCTATCTATCTATCTATCTATCATCTATCTAGCTAGCTATCTATCTATAGAAC
TAATGGGGAGGGTTTACCATGTTTGGGTGAACCCAAACATTTTATGGNCAAGGGNTT
GGAAAATTACCCTTATCTACAACNTTNAACCTTGTTTTGGTAGGNGTGNTAATTCCN
TGGGNTTGGGAANAACCTTTGNAATTCCTCNTTGTNTNTNATTNNNNATTNNTNNNC
ATTATTNTGGGGTNTTCNGGGTGGAGGGCTNANTTTGGCCNCCCGGGTCCNNGGNG
CNAGTNGGNNNGGNTNNTNGGGTTTNCCTGGGAANCNTNCCNCCTNCNGGGGNTTC
ANGGGNTTTTTNTTTNNTTG {(SEQ ID NO:89)}

Genbank ID: G09963

Description: human STS CHLC.GATA61E10.P17745 clone GATA61E10.

Search for GDB entry

GCT3G01:

Database ID: GCT-P10825 (Also known as G09484, CHLC.GCT3G01, CHLC.GCT3G01.P10825)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:

Left = CTTTGCAATCTTAGTTAATTGGC {(SEQ ID NO:90)}

Right = GAACTATGATATGGAGTAACAGCG {(SEQ ID NO:23)}

Product Length = 128

Review complete sequence:

AGATGTTTAACTTTGCAATCTTAGTTAATTGGCAGAAATGAAATTTAGTTTCCACAA
CTTTTATTCGATATTAACACACCACCACCATCAGCAGCAGCAGCAGCAGCAGCAGC
ATCGCTGTTACTCCATATCATAGTTTCAGAGCATTTAAAGNNGGTCAAAATATACAAC
AGGCTGACACCNGNATAAGGTTTAATTTTAAACCNGNGGTCTNCCCTCTAAGGNGG
NTTTTTTTTTCTTGNCNTGGCTTCTTTTTCCNTTGTCTTTGTAAAATATCAAGGNATT
TTTGGGTTNTTCNTGGNANTTNNCANNANTNNTNNTTNNNCNCNCCCCCCTTTGNGG
CGGGGGTCCCNNTTGTCCCGGGGTGNGTGCAGTAGGGGGGTNCNCGGGTNNNGN
AAGTTTNGGGGCCCT {(SEQ ID NO:91)}

Genbank ID: G09484

Description: human STS CHLC.GCT3G01.P10825 clone GCT3G01.

WI-528:

Database ID: MH232 (Also known as G03589, 528, D18S828)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = TTCTGCCTTTCCTGACTGTC {(SEQ ID NO:92)}

Right = TGTTTCCCATGTCTTGATGA {(SEQ ID NO:93)}

Product Length = 211

Review complete sequence:

CTACTAAGCAAATTCTGCTCAGCCTTCTGCCTTTCCTGACTGTCTTGTTGGCCCTTCC
CACTTTAAGGATGCCTGTTTAAGTAGCCACCTCTAATTAGGAATCTTCCCTTGTTCTT
TCTCAGGAGGCTTAGACACTGTCAGTTTCCTGAAGACAGAAAATAAGCCTGCATTAT
CCTAGTAGTGGATTCAAACTAATTGTGTCCTGAGTCTTCAATCATCAAGACATGG
GAAACACTCAACAG {(SEQ ID NO:94)}

Genbank ID: G03589

Description: WICGR: Random genome wide STSs

Search for GDB entry

25. WI-1783:

Database ID: MR432 (Also known as G03587, _shu_31.Seq, 1783, D18S824)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = CCAGTAATTAGACATTGACAGGTTC {(SEQ ID NO:95)}

Right = TTTTACTAGACAGGCTTGATAAACAA {(SEQ ID NO:96)}

Product Length = 305

Review complete sequence:

CCAGTAATTAGACATTGACAGGTTCCATACTAGTAATGTAGGGAATAGGGCTGCTGC
TTTTTGGGTTTCCTTGAGTATACTTTGTGCTGCATAAATATGGCAATGGATAGTAAAT
AATTTGTATGCAGACCTTTAGTGTCTGATTAACTGTGAATAAGGGAACAACAATCAA
GGACAAAAATCAAAAGACTAATTCTCTATACATTTTGAGCTTTTGTAAGTAAGTAAG
ATTAGCTGAATATATCTGAAAAATTTCTAATCTCCTTTACAATTTTTTAAATTGTTTA
TCAAGCCTGTCTAGTAAAAATAATTCAGTTTCGGAATGTGG {(SEQ ID NO:97)}

Genbank ID: G03587

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S477:

Database ID: AFM301XF5 (Also known as 301xf5, Z24212, D18S477)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = GGACATCCTTGATTTGCTCATAA {(SEQ ID NO:98)}

Right = GATTGACTGAAAACAGGCACAT {(SEQ ID NO:99)}

Product Length = 243

Review complete sequence:

GGACATCCTTGATTTGCTCATAATACACTCATTCCTTTCACCATTGAGTGTGCACATA
TTTCTCTGATTGGAAAGAACTACAGAGGAGGTTTTACNTTTTACTTTCCAGTTTGCTA
TTAAAGAGAGAAAACTAACAGAGNGAAATCAAGCAACTCAAAACAACCTTACACAC
ACACACACACACACACTCACAAAGATATTTTGTTTACCATATGTATTGATGTGCC
TGTTTTCAGTCAATCCACAGGAAGGGCTAAGGAGAGTGACATCTGGGCTACATTAA
AAGGACAGTCACATTGCTCAAAGNACTCAAGTTTAGCCCGAGTACAGTAGCT {(SEQ
ID NO:100)}

Genbank ID: Z24212

Description: H. sapiens (D18S477) DNA segment containing (CA) repeat; clone

Search for GDB entry

D18S979:

Database ID: GATA-P28080 (Also known as G08015, CHLC.GATA92C08, CHLC.GATA92C08.P28080)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:

Left = AGCTTGCAGATAGCCTGCTA {(SEQ ID NO:101)}

Right = TACGGTAGGTAGGTAGATAGATTCG {(SEQ ID NO:102)}

Product Length = 155

Review complete sequence:

CTCTACAGTCTCTNACCTTTGGACTCCAGGACTTTACCAGCACCTCAACATTCCCA
CTGGGTTCTCAGGACTTTATAGTTGTACTGAGCCATGCCACTGGATCCTAGGGTCTC
CAGCTTGCAGATAGCCTGCTATGGGACTTAATCTTTGTAATAAGGTGAGTCAATTCT
GCCAATAAACCTACTTTCATCTCTATCTATCTATCTATCTATCTATCTATCTATA
TCTATCATCTATCTATCGAATCTATCTACCTACCTACCGTATTAGTTCTGTCTCTCTGG
AGN {(SEQ ID NO:103)}

Genbank ID: G08015

Description: human STS CHLC.GATA92C08.P28080 clone GATA92C08.

WI-9340:

Database ID: UTR-05134 (Also known as G06102, D18S1034, 9340, X60221)

Source: WICGR: Primers derived from Genbank sequences

Chromosome: Chr18

Primers:

Left = TGAGAGAACGAAATCTCTATCGG {(SEQ ID NO:104)}

Right = AGGCAGCAAGTTTTATAAAGGC {(SEQ ID NO:105)}

Product Length = 115

Review complete sequence:

ATGTATCTATCCCAATTGAGTCAGCTAGAAACAGTTGACTGACTAAATGGAACTAG
TCTATTTGACAAAGTCTTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTACCCTTCCT
AAAAATGAAAAGTTTGTTCATATAGTGAGAGAACGAAATCTCTATCGGCCAGTCA
GATGTTTCTCATCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCATTCTGAATAAG
CATTTGCCTTTATAAAAACTTGCTGCCTGACTAAAGATTAACAGGTTATAGTTTAAA
TTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAATG {(SEQ ID NO:106)}

Genbank ID: G06102

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S466:

Database ID: AFM094YE5 (Also known as 094ye5, Z23354, D18S466)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:

Left = ACACTGTAGCAGAGGCTTGACC {(SEQ ID NO:107)}

Right = AGGCCAAGTTATGTGCCACC {(SEQ ID NO:108)}

Product Length = 214

Review complete sequence:

aaatgacactttaaggaggtaacactgtagcagaggcttgaccaccaccagttctactagcactgaggatgctctattggttgggttacc
acacacgcatagacatgcacacacagacacacagacacacacacacacacacacaccagatatagcattccaaacctcaatatgc
tatgcaatactgcattaacagggtcatgcctgtggtggcacataactggcctagaaaatactggggacgtctgcattccctttattatcgaattg
acttacttggtctctgagtttctcagaagtaacttcaatacctcttcattctgccttgancattgttgggtaccaagtatagct {(SEQ
ID NO:109)}

Genbank ID: Z23354

Description: H. sapiens (D18S466) DNA segment containing (CA) repeat; clone

Search for GDB entry

D18S1092:

Database ID: AFMA112WE9 (Also known as D18S1092, w5374, a112we9)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = CTCTCAAAGTAAGAGCGATGTTGTA {(SEQ ID NO:110)}

Right = CCGAAGTAGAAAATCTTGCA {(SEQ ID NO:111)}

Product Length = 163

Review complete sequence:

agctctcaaagtaagagcgatgttgaactgactgagttgtttgtgaantttgntttggagtcagtgaggcatgttattagatgtaaattaaac
acacacacacacacacacacacacacacacagagaagtaagtccaagattttctacttcggcgccctatattctatatactgattttctgtatttc
ccagacttgaatatagattgtctttctgntttatcatagacaatctcataaanttaggcataataaggtaatgaggntttctgggcttctttcat
catccctgcaatttgagtcctnttatagntgaantcttctctgtaataentcttgttttagct {(SEQ ID NO:112)}

Search for GDB entry

D18S61:

Database ID: AFM193YF8 (Also known as 193yf8, Z16834, D18S61)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = ATTTCTAAGAGGACTCCCAAAC {(SEQ ID NO:113)}

Right = ATATTTTGAACTCAGGAGCAT {(SEQ ID NO:114)}

Product Length = 174

Review complete sequence:

CGTCTTACCAAACCAACATAATATAGCAATGGNAACCAAAAATTTCTAAGAG
GACTCCCAAACCTACATTCTTCTNCCTGAATTAAATACAGGCATTCAANANAAACANA
CACACACACACACACACACACACACACACACACACGCACACCCTTCAAATCNTA
GCATAAATTCCNCTTATATAAACATAACCATGCTCCTGAGTTTCAAAATATTGGGTG
GTTCTGAAGTTCGAAGCAACAAATTTCCAGTTAGTGTCTATTANTTGTGGACAGCT
{(SEQ ID NO:115)}

Genbank ID: Z16834

Description: H. sapiens (D18S61) DNA segment containing (CA) repeat; clone

Search for GDB entry

Markers (STRs) used in refining the candidate region.

Below the markers are shown that were used in family MAD31 to refine the candidate region. Most of these markers are already described above and will therefore only be mentioned to by their name. For the additional markers, the information is given here.

Data was already shown for: D18S68, D18S55, D18S969, D18S1113, D18S483, D18S465, D18S876, D18S477, D18S979, D18S466 and D18S61.

New data:

D18S51:

Other names: UT574, (D18S379)

Primer sequences:

UT574a GAGCCATGTTTCATGCCACTG {(SEQ ID NO:116)}

UT574b CAAACCCGACTACCAGCAAC {(SEQ ID NO:117)}

DNA-sequence:

AATTGAGCNCAGGAGTTTAAGACCAGCCTGGGTAACACAGTGAGACCCCTGT
CTCTACAAAAAATACAAAAATNAGTTGGGCATGGTGGCACGTGCCTGTAGTCTCA
GCTACTTGCAGGGCTGAGGCAGGAGGAGTTCTTGAGCCCAGAAGGTTAAGGCTGCA
GTGAGCCATGTTTCATGCCACTGCACTTCACTCTGAGTGACAAATTGAGACCTTGTCT
CAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA
GTAAGAAAAAGAGAGGGAAAGAAAGAGAAANAGNAAANAAATAGTAGCAACTGTT
ATTGTAAGACATCTCCACACACCAGAGAAGTTAATTTTAATTTTAACATGTTAAGAA
CAGAGAGAAGCCAACATGTCCACCTTAGGCTGACGGTTTGTTTATTTGTGTTGTTGCT
TGGTAGTCGGGTTTGTTATTTTAAAGTAGCTTATCCAATACTTCATTAACAATTTCA
GTAAGTTATTTTCATCTTTCAACATAAATACGNACAAGGATTTCTTCTGGTCAAGACC
AAACTAATATTAGTCCATAGTAGGAGCTAATACTATCACATTTACTAAGTATTCTAT
TTGCAATTTGACTGTAGCCCATAGCCTTTTGTCGGCTAAAGTGAGCTTAATGCTGATC
GACTCTAGAG {(SEQ ID NO:118)}

GENBANK ID: L18333

D18S346.

Other name: UT575

Primer Pairs:

Primer A: TGGAGGTTGCAATGAGCTG {(SEQ ID NO:119)}

Primer B: CATGCACACCTAATTGGCG {(SEQ ID NO:120)}

DNA sequence:

ACGAGGACAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCCCGTTTNTACTA
AAANTACAAAANTTGGTCGGGAGGCTGGGGCAGGNGACATGCTTGACCCCAGGAGG
TGGAGGTTGCAATGAGCTGAGATTGCACCACTGCACTNCAGCNTGG. {(SEQ ID
NO:121)}.....AAGAAAGAGAAAGGANAGNNAGGNAGNNANNAACTACATNTGAAGT
CAACACTAGTATTGGTGGGAGAGGAATTTTATGCTGCATTCCCNACAACCACTAGA
TACGCCAATTAGGTGTGCATGGTCCATGCTAT {(SEQ ID NO:122)}

GenBank ID: L26588

D18S817.

Other name: UT6365

Primer Pairs:

Primer A: GCAAAGCAGAAGTGAGCATG {(SEQ ID NO:123)}

Primer B: TAGGACTACAGGCGTGTGC {(SEQ ID NO:124)}

DNA Sequence:

CATATGGGTCCACAAGCAACCTCAGTCCTTGTCTCTTCAGAAGAAAGAATTCTACTG
AGGGNCATAAGGCAGAAGGAGAGACCTAGGCAAGTTGCAAAGCAGAAGTGAGCAT
GTATTA AAAAGCTTTAGAACAGTAAGGAAAGGAAGAAAAGAAAAGAAGGAAAGTT
CAACTTGGAAGAGGGCCAAGCCGGCAACTTGGCAGAAGGATTGCTTGAGCCCAGGA
GTTAAGACCAGTCTGGGCAATATAGTGAGACTCCATCTCTGCATACATACATACATA
CATACATACATACATACATACATATTTGCAGGGTATGATGGCACACGCCTGTAG
TCCTAGCTACTCTGGAGGTTGAGATGGGAGGGTCACTGAGCCTGGGAANTTGAGGC
TGCNNTGAGCCATGATC {(SEQ ID NO:125)}

GenBank ID: L30552

Characterisation of YACs.

8 YACs were selected covering the candidate region and flanking the gap. These YACs were further characterised by determining the end-sequences by the Inverse-PCR protocol.

Selected YACs: 961_h_9, 942_c_3, 766_f_12, 731_c_7, 907_e_1, 752_g_8, 717_d_3, 745_d_2

New STSs based on end-sequences (unless indicated otherwise, the STSs were tested on a monochromosomal mapping pannel for identifying chimaerism of the YAC; if the STS revealed a hit not on chromosome 18q -chimaeric YAC- then it is indicated in the text below):

SV32L.

Derived from YAC 745_d_2 left arm end-sequence.

Primer A: GTTATTACAATGTCACCCTCATT {(SEQ ID NO:126)}

Primer B: ACATCTGTAAGAGCTTCACAAACA {(SEQ ID NO:127)}

DNA-sequence:

ATTCCTTNGTTATTACAATGTCACCCTCATTTAAAAAGTGGAAGATAAAGAGGAAG
CAATCTATTTTTTCTTTTTTCTGATAGCACTTGTTTGTGAAGCTCTTACAGATGTT
CTTAAGTAAAATCAACTCCTCCATTTTTTTGTAGCAACTACACATATTTATCAATAA
TAGTTCACAAATACATTTTCAAATT {(SEQ ID NO:128)}

Amplified sequence length: 107 basepairs (bp)

This STS has no clear hit on the monochromosomal mapping pannel.

SV32R.

Derived from YAC 745_d_2 right arm end-sequence.

Primer A: ACGTTTCTCAATTGTTTAGTC {(SEQ ID NO:129)}

Primer B: TGTCTTGGCATTATTTTAC {(SEQ ID NO:130)}

DNA sequence:

AGACAATGGGAGAAATTGCACTGCCCTGAGTCAGAAATCAGATCTGTTGCCATACA
GCTGCCGTTATGTGATCATTTGCAAGTCAACGTTTCTCAATTGTTTAGTCATTTGTAA
GACAAAAAGACTGGTTGGATTTCAGAGAATTTGGAATCCTCCTTCAGGTTTAAACAAG
CAATAAATGATACTCTTCAGTGTAATAATAATGCCAAGACATNATTTGACTTTAAAT
TAAATCCAAACAAGATATC {(SEQ ID NO:131)}

Amplified sequence length: 127 bp

This STS has no clear hit on the monochromosomal mapping pannel.

SV11L.

Derived from YAC 766_f_12 left arm end-sequence.

Primer A: CTATGCTCTGATCTTTGTTACTTT {(SEQ ID NO:132)}

Primer B: ATTAACGGGAAAGAATGGTAT {(SEQ ID NO:133)}

DNA sequence:

GTCTTTATTTTCATATAACTATGCTCTGATCTTTGTTACTTTCTCCTTTTAACTCAGTTT
AAGCTTTATTCTTATTTTCCAGCTGCTGAAGGTATATAGTTAGGTTGTTTATTGGATA
CCATTCTTTCCCGTTAATGTCAGTGGTACTGCTATCAATGTAGCAGTTA {(SEQ ID
NO:1)}

Amplified sequence length: 118 bp

This STS has a hit with chromosome 18 and must be located between CHLC.GATA-p6051 and D18S968.

SV11R.

Derived from YAC 766_f_12 right arm end-sequence.

Primer A: AAGGTATATTATTTGTGTCG {(SEQ ID NO:134)}

Primer B: AAACCTTTCTTAACCTCATA {(SEQ ID NO:135)}

DNA sequence:

ATAAGGTATATTATTTGTGTCGTGAGTTAAGAAATCATTAATAACTATTTTCAGAAT
GACAAATGTCATTATATGTTGTAAAAAAGATAAATACGTGAAATTATGAGGTTAAG
AAAAGTTTA {(SEQ ID NO:2)}

Amplified sequence length: 119 bp.

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01.

SV34L.

Derived from YAC 717_d_3 left arm end-sequence.

Primer A: TCTACACATATGGGAAAGCAGGAA {(SEQ ID NO:136)}

Primer B: GCTGGTGGTTTTGGAGGTAGG {(SEQ ID NO:137)}

DNA sequence:

ACATAAAATGTCGCTCAAAAACAATTATGTGTGTCTACACATATGGGAAAGCAGGA
AACAAATTTGTTTACAACATACATTACTTTTGTTTTTTAGGCAAGATAAAATNTCCTA
CCTCCAAAACCAACGACACNGTCCGCAATAACTATACATC {(SEQ ID NO:3)}

Amplified sequence length: 98 bp

This STS has a hit with chromosome 18.

SV34R.

Derived from YAC 717_d_3 right arm end-sequence.

Primer A: ATAAGAGACCAGAATGTGATA {(SEQ ID NO:138)}

Primer B: TCTTTGGAGGAGGGTAGTC {(SEQ ID NO:139)}

DNA-sequence:

AATATCATTCTTCACCCACGTTATACATAAGAGACCAGAATGTGATATTGTCATCTC
ACATGGAAAAATCTGCTGTGATCAGTTCCTGAAGCTTGCTGTGATCCTCCCTTAGGA
AAGTAGAAAAATCTTTTGAACACTTTATTCTACAATCAATGAAAATTAGGTGAAG
CTACAGAAGCCAGAAATTACTCTAAGATTAGACAATTATTTAAGANGACCAATTGTC
TTTGGTCTTCTTCTGAAGGGTCTGACTACCCTCCTCCAAAGAATTCAGTGGCCGTCGT
TTTACAACGTCNTGA {(SEQ ID NO:4)}

Amplified sequence length: 244 bp

This STS has a hit with chromosome 1, therefore YAC 717_d_3 is chimaeric

SV25L.

Derived from YAC 731_c_7 left arm end-sequence.

Primer A: AAATCTCTTAAGCTCATGCTAGTG {(SEQ ID NO:140)}

Primer B: CCTGCCTACCAGCCTGTC {(SEQ ID NO:141)}

DNA sequence:

AGTGGAGAGATAGAAAGAGAGGAAGATTTTTTTTTTTAAATCTCTTAAGCTCATGCT
AGTGTAGGTGCTGGCAGGTCTGAACACTCTGTAGGACAGGCTGGTAGGCAGGAA
{(SEQ ID NO:142)}

Amplified sequence length: 72 bp

This STS has no clear hits on the monochromosomal mapping pannel.

SV25R.

Derived from YAC 731_c_7 right arm end-sequence.

Primer A: TGGGGTGCCTGTGTTGT {(SEQ ID NO:143)}

Primer B: GAGATTTTCATGCATTCCTGTAAGA {(SEQ ID NO:144)}

DNA-sequence:

GGAGGGTGTNTCACANAAGTCTGGGGTGCCTGTGTTGTTTCATTGTAAAAACCCTT
TGGANCATCTGGGAATGTGCTGCCCCACATGTCCAGGTAACGTTCTCAGGAAGGGG
AGGCTGGAAATCTCTGTGTGTTCTTACAGGAATGCATGAAATCTCCCANCCCCCTCTT
GTTGGAAATTTCCCTCACTTT {(SEQ ID NO:5)}

Amplified sequence length: 136 bp

This STS has a hit with chromosome 7; therefore YAC 731_c_7 is chimaeric

SV31L.

Derived from YAC 752_g_8 left arm end-sequence.

Primer A: GAGGCACAGCTTACCAGTTCA {(SEQ ID NO:145)}

Primer B: ATTCATTTTCTCATTTTATCC {(SEQ ID NO:146)}

DNA-sequence:

CTTCTCNATGANTGGACAAATGTCATTGGGTCAGCATGAGGCACAGCTTACCAGTTC
AGATTCCAGTAGCTGAGGAACAAATCTTAACCTCAAAAATAAGTAATTGCGTCACTT
TGGAGGAATTATTGACCTTTTCATAACTTTGACATCACAACAATGAGGGTGAAGTT
AGTAAAATAAATGATTATTATGAGGATAAAATGAGAAAATGAATTNAGTGCTTAAG
ACAATGCTTGGTAACTAGTTAANCCG {(SEQ ID NO:6)}

Amplified sequence length: 178 bp

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01.

SV31R.

Derived from YAC 752_g_8 right arm end-sequence.

Primer A: CAAGATTATGCCTCAACT {(SEQ ID NO:147)}

Primer B: TAAGCTCATAATCTCTGGA {(SEQ ID NO:148)}

DNA sequence:

AAACTTTAACCAATTTAAACTCCCTAACAGTTCTATAAAATAAGCAAGATTATGCCT
CAACTTTTATGGATAAAGAAATGGAGGCATTAAGAGATAACTAACTTGCCCAAGGCC
ACACAAGTGACTGAGTAAGAATTGCAAAGCCAATGAGTCTGGCTCCAGAGATTATG
AGCTTAATCACCACACTGTGCCACCTCCTGTGTTTCCTGG {(SEQ ID NO:149)}

Amplified sequence length: 131 bp

This STS has no clear hits on the monochromosomal mapping pannel and gives no information concerning the chimaerity of the YAC.

SV10L.

Derived from YAC 942_c_3 left arm end-sequence.

Primer A: TCACTTGGTTGGTTAACATTACT {(SEQ ID NO:150)}

Primer B: TAGAAAAACAGTTGCATTTGATAT {(SEQ ID NO:151)}

DNA-sequence:

GGTNTTTCACTTGGTTGGTTAACATTACTTCTAAGTTTTTTATTGTTTTTTATGCTATT
GCTAATGGGATTGCTTTCTTAATTTATTTTTTCCAATAGCTTGTTGTTAGTTTATATCA
AATGCAACTGTTTTTCTATGCAAATTATGTTTCCT {(SEQ ID NO:7)}

Amplified sequence length: 130 bp

This STS has a hit with chromosome 18 and must be located between CHLC.GATA-p6051 and D18S968

SV10R.

Derived from YAC 942_c_3 right arm end-sequence.

Primer A: AACCCAAGGGAGCACAACCTG {(SEQ ID NO:152)}

Primer B: GGCAATAGGCTTTCCAACAT {(SEQ ID NO:153)}

DNA sequence:

TTGGTGGTGCCCTAGGTTTGGCAATTATAAATAAAGCTGCTACAAACATTCATGTGC
AGGTCTCCGTGTGGACATAATTTCCAGTTCATTTGGGTAAAACCCAAGGGAGCACA
ACTGTTGGATCCTATNATAAAAAATATNTCTCGTTTCATTTAACCTGGGAAACT
ATCTNCCCACAGTGGCTGTCCCTTTTGTATCCCCACCAACAATGTTGGAAAGCCTAT
TGCCANCAT {(SEQ ID NO:8)}

Amplified sequence length: 135 bp

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01

SV6L.

Derived from YAC 961_h_9 left arm end-sequence.

No primer was made, because this sequence is identical to a known STR marker D18S42, which is indeed mapped to this region.

Primer A:

Primer B:

DNA sequence:

CATGNCTCACAGTGTCTGAGGCTGCTCTGGACATGCAATCTTGCATGCTTTTGTCAT
GACAGGTCTTAAANAGTTTATCAGCTTNCTCAAATAGCTGAATGACANAACACTGG
ATTTTGTTCAAATANCCTATCAACTTGGCNTCTGTGTTGCGGTTGTCACTTGGTAAC
AAAATAAGTC {(SEQ ID NO:9)}

Amplified sequence length:

SV6L recognises D18S42 which must be therefore located between WI-7336 and WI-8145

SV6R.

Derived from YAC 961_h_9 right arm end-sequence.

Primer A: TTGTGGAATGGCTAAGT {(SEQ ID NO:154)}

Primer B: GAAAGTATCAAGGCAGTG {(SEQ ID NO:155)}

DNA sequence:

TAATTGACAAATAAAAATTGTATATTTTNCATATTTAACATGTTATGCTAACATATAT
ATGGATTGTGGAATGGCTAAGTCAGAAATTCCTTTACATTCATATTTCCATATTATTT
ACTTTNNGCTTTAAAAAATATGTAAATGANAATACTTATTTTTTTTCAGTGTCACTGCC
TTGATACTTTTACATTTNNGTTACATATTATTTCCCTTNCATCTAACAAATATATATT
GAGTTTCTATAATGTGTCTGACACTGA {(SEQ ID NO:10)}

Amplified sequence length: 122 bp

SV6R amplifies a segment on chromosome 18. This segment must be located between WI-2620 and WI-4211

SV26L.

Derived from YAC 907_e_1 left arm end-sequence.

Primer A: TATTTGGTTTGTGCTGAGGT {(SEQ ID NO:156)}

Primer B: CAAGAAGGATGGATACAAACAAG {(SEQ ID NO:157)}

DNA sequence:

TGGTCACTGGTGCCTTTATTTGGTTTGTGCTGAGGTCATATTCCTGTGGCCTTCAT
GCTTGATTTGTTGGAGTCTAGCCATGTAAAANTCTGTTGGAGTCTAGGCATTAAAA
AATAGGTATTTATTGTAATCTTTGCCATTTGCTTGTTTGTATCCATCCTTCTTGGA
GGCTTTACAGGCATTCAAAGG {(SEQ ID NO:11)}

Amplified sequence length: 154 bp

This STS has a hit with chromosome 13; therefore YAC 907_e_1 is chimaeric.

SV26R.

Derived from YAC 907_e_1 right arm end-sequence.

Primer A: CGCTATGCATGGATTTA {(SEQ ID NO:158)}

Primer B: GCTGAATTTAGGATGTAA {(SEQ ID NO:159)}

DNA sequence:

CGCTATGCATGGATTTAAACTGAGTGTAGTGCCTCACTATGTTGCAGTCTCTTATTC
TAGGTTCCTAATATTTACATCCTAAATTCAGCT {(SEQ ID NO:160)}

Amplified sequence length: 90 bp

no clear hits on monochromosomal mapping pannel: no information concerning chaemerity at this side of the YAC

Page 64, line 5 through line 19:

A 4.5kb ECORI/SalI fragment of pBLC8.1 (Lewis *et al*, 1992) carrying a lysine-2 and a telomere sequence was directionally cloned into GEM3zf(-) digested with ECORI/SalI.

Subsequently, an End Rescue Site was ligated into the EcoRI site. Hereto, two oligonucleotides (strand 1: 5'-TTCGGATCCGGTACCATCGAT-3' {(SEQ ID NO:161)} AND STRAND 2: 3'GCCTAGGCCATGGTAGCTATT-5' {(SEQ ID NO:162)}) were ligated into a partial (dATP) filled ECORI site, generating the vector pDF1. Triplet repeat containing fragmentation vectors were constructed by cloning of a 21bp and a 30bp CAG/CTG adapter into the Klenow-filled PstI site of pDF1. [Trasformation] Transformation and selection resulted in a (CAG)₇ and a (CTG)₁₀ fractionation vector with the orientation of the repeat sequence 5' to 3' relative to the telomere.